

STN Search Summary 10/620,487

=> d his

(FILE 'HOME' ENTERED AT 13:19:23 ON 25 JAN 2005)

FILE 'CAPLUS' ENTERED AT 13:21:04 ON 25 JAN 2005

L1 6 S YFIK
L2 134 S s (RhtB or ydeD or yedA or lysE or pecm or thrE) (s) (increas? or ehanc?)
L3 24 S L2 (S) (ACTIVIT? OR EXPRESSI? OR (COPY W NUMBER))
L4 2 S L3 (P) (MICROORGANSIM? OR COLI? OR ESCHERICHIA? OR BACTERI?)
L5 2 s L3 (p) (microorgansim? or coli? or escherichia? or bacteri? or yeast or fungus or enterobacteriaceae)
L6 3 s l3 and (phosphoglycerate or ?serine? or ?cysteine? or ?cystine? or ?glycine) and fermentati?

s l3 and (phosphoglycerate or ?serine? or ?cysteine? or ?cystine? or ?glycine) and fermentati?

=> s yfiK

L1 6 YFIK

=> d l1 1-6

X L1 ANSWER 1 OF 6 CAPLUS COPYRIGHT 2005 ACS on STN
AN 2004:131333 CAPLUS
DN 140:248969
TI High level cell-free expression and specific labeling of integral membrane proteins
AU Klammt, Christian; Loehr, Frank; Schaefer, Birgit; Haase, Winfried; Doetsch, Volker; Rueterjans, Heinz; Glaubitz, Clemens; Bernhard, Frank
CS Centre for Biomolecular Magnetic Resonance, Institute for Biophysical Chemistry, University of Frankfurt/Main, Frankfurt/Main, Germany
SO European Journal of Biochemistry (2004), 271(3), 568-580
CODEN: EJBCAI; ISSN: 0014-2956
PB Blackwell Publishing Ltd.
DT Journal
LA English
RE.CNT 44 THERE ARE 44 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

App L1 ANSWER 2 OF 6 CAPLUS COPYRIGHT 2005 ACS on STN
AN 2004:55470 CAPLUS
DN 140:127258
TI Fermentative production of amino acids of the phosphoglycerate family by Escherichia coli overexpressing gene yfiK
IN Maier, Thomas
PA Consortium fuer Elektrochemische Industrie GmbH, Germany
SO Eur. Pat. Appl., 16 pp.
CODEN: EPXXDW
DT Patent
LA German
FAN.CNT 1

| | PATENT NO. | KIND | DATE | APPLICATION NO. | DATE |
|--------|---|--|----------|------------------|----------|
| PI | EP 1382684 | A1 | 20040121 | EP 2003-15546 | 20030710 |
| | R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR, BG, CZ, EE, HU, SK | | | | |
| | DE 10232930 | A1 | 20040205 | DE 2002-10232930 | 20020719 |
| | US 2004038352 | A1 | 20040226 | US 2003-620487 | 20030716 |
| | CA 2433485 | AA | 20040119 | CA 2003-2433485 | 20030717 |
| | JP 2004049237 | A2 | 20040219 | JP 2003-199397 | 20030718 |
| | CN 1487079 | A | 20040407 | CN 2003-178667 | 20030718 |
| PRAI | DE 2002-10232930 | A | 20020719 | | |
| RE.CNT | 5 | THERE ARE 5 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT | | | |

L1 ANSWER 3 OF 6 CAPLUS COPYRIGHT 2005 ACS on STN
 AN 2003:116387 CAPLUS
 DN 138:334174
 TI YfiK from Escherichia coli promotes export of O-acetylserine and cysteine
 AU Franke, Isabel; Resch, Armin; Dassler, Tobias; Maier, Thomas; Bock, August
 CS Department Biologie I, Mikrobiologie, Universitat Munchen, Munich, Germany
 SO Journal of Bacteriology (2003), 185(4), 1161-1166
 CODEN: JOBAAY; ISSN: 0021-9193
 PB American Society for Microbiology
 DT Journal
 LA English
 RE.CNT 32 THERE ARE 32 CITED REFERENCES AVAILABLE FOR THIS RECORD
 ALL CITATIONS AVAILABLE IN THE RE FORMAT

L1 ANSWER 4 OF 6 CAPLUS COPYRIGHT 2005 ACS on STN
 AN 2001:880292 CAPLUS
 DN 136:336109
 TI Comprehensive DNA microarray analysis of Bacillus subtilis two-component regulatory systems
 AU Kobayashi, Kazuo; Ogura, Mitsuo; Yamaguchi, Hirotake; Yoshida, Ken-Ichi; Ogasawara, Naotake; Tanaka, Teruo; Fujita, Yasutaro
 CS Graduate School of Biological Sciences, Nara Institute of Science and Technology, Nara, 630-0101, Japan
 SO Journal of Bacteriology (2001), 183(24), 7365-7370
 CODEN: JOBAAY; ISSN: 0021-9193
 PB American Society for Microbiology
 DT Journal
 LA English
 RE.CNT 27 THERE ARE 27 CITED REFERENCES AVAILABLE FOR THIS RECORD
 ALL CITATIONS AVAILABLE IN THE RE FORMAT

L1 ANSWER 5 OF 6 CAPLUS COPYRIGHT 2005 ACS on STN
 AN 2000:456755 CAPLUS
 DN 133:85119
 TI Production of L-amino acids by bacterium transformed with amino acid excretion protein homologs
 IN Livshits, Vitaliy Arkadievich; Zakataeva, Natalia Pavlovna; Nakanishi, Kazuo; Aleshin, Vladimir Veniaminovich; Troshin, Petr Vladimirovich; Tokhmakova, Irina Lyvovna
 PA Ajinomoto Co., Inc., Japan
 SO Eur. Pat. Appl., 29 pp.
 CODEN: EPXXDW

DT Patent
LA English
FAN.CNT 1

| | PATENT NO. | KIND | DATE | APPLICATION NO. | DATE |
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| | ----- | ---- | ----- | ----- | ----- |
| PI | EP 1016710 | A2 | 20000705 | EP 1999-125263 | 19991217 |
| | EP 1016710 | A3 | 20000906 | | |
| | R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO | | | | |
| | RU 2175351 | C2 | 20011027 | RU 1999-104431 | 19990309 |
| | AU 9964493 | A1 | 20000706 | AU 1999-64493 | 19991213 |
| | AU 764189 | B2 | 20030814 | | |
| | ZA 9907767 | A | 20000630 | ZA 1999-7767 | 19991220 |
| | JP 2000189180 | A2 | 20000711 | JP 1999-373651 | 19991228 |
| | BR 9906287 | A | 20010123 | BR 1999-6287 | 19991228 |
| | KR 2000048465 | A | 20000725 | KR 1999-64627 | 19991229 |
| | CN 1261626 | A | 20000802 | CN 1999-127522 | 19991230 |
| PRAI | RU 1998-124016 | A | 19981230 | | |
| | RU 1999-104431 | A | 19990309 | | |

L1 ANSWER 6 OF 6 CAPLUS COPYRIGHT 2005 ACS on STN
AN 1996:737199 CAPLUS
DN 126:100025
TI The Bacillus subtilis chromosome region near 78° contains the genes
encoding a new two-component system, three ABC transporters and a lipase
AU Yamamoto, Hiroki; Uchiyama, Shigeki; Sekiguchi, Junichi
CS Department of Applied Biology, Faculty of Textile Science, Technology,
Shinshu University, 3-15-1 Tokida, Ueda-shi, Nagano, 386, Japan
SO Gene (1996), 181(1/2), 147-151
CODEN: GENED6; ISSN: 0378-1119
PB Elsevier
DT Journal
LA English

=> d 14

L4 ANSWER 1 OF 2 CAPLUS COPYRIGHT 2005 ACS on STN
AN 2003:417877 CAPLUS
DN 139:2051
TI Over expressing E. coli yedA gene for
increase the yield of producing of L-amino acid and its
derivatives
IN Livshits, Vitaliy Arkadyevich; Vitushkina, Maria Viacheslavovna;
Gusyatiner, Mikhail Markovich; Ziyatdinov, Mikhail Kharisovich;
Akhverdian, Valery Zavenovich; Savrasova, Ekaterina Alekseevna;
Doroshenko, Vera Georgievna; Mashko, Sergey Vladimirovich
PA Ajinomoto Co., Inc., Japan
SO PCT Int. Appl., 28 pp.
CODEN: PIXXD2
DT Patent
LA Japanese
FAN.CNT 1

| | PATENT NO. | KIND | DATE | APPLICATION NO. | DATE |
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| | ----- | ---- | ----- | ----- | ----- |
| PI | WO 2003044191 | A1 | 20030530 | WO 2002-JP12202 | 20021121 |
| | W: AU, BR, BY, CA, CN, HU, IL, IN, JP, KR, MX, NO, PL, UA, VN, ZA | | | | |
| | RW: AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, | | | | |
| | LU, MC, NL, PT, SE, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, | | | | |
| | GW, ML, MR, NE, SN, TD, TG | | | | |
| | RU 2229513 | C2 | 20040527 | RU 2001-131570 | 20011123 |
| | EP 1449917 | A1 | 20040825 | EP 2002-788635 | 20021121 |
| | R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, | | | | |
| | IE, FI, CY, TR, BG, CZ, EE, SK | | | | |
| | US 2003148473 | A1 | 20030807 | US 2002-302983 | 20021125 |
| PRAI | RU 2001-131570 | A | 20011123 | | |
| | WO 2002-JP12202 | W | 20021121 | | |
| RE.CNT | 10 | THERE ARE 10 CITED REFERENCES AVAILABLE FOR THIS RECORD | | | |
| | | ALL CITATIONS AVAILABLE IN THE RE FORMAT | | | |

=> d 14 2

L4 ANSWER 2 OF 2 CAPLUS COPYRIGHT 2005 ACS on STN
AN 2003:266869 CAPLUS
DN 138:266848
TI Arginine repressor deficient strain of Escherichia or coryneform bacteria
with LysE gene overexpression for L-arginine production
IN Yamaguchi, Mikiko; Ito, Hisao; Gunji, Yoshiya; Yasueda, Hisashi
PA Ajinomoto Co., Inc., Japan
SO Jpn. Kokai Tokkyo Koho, 36 pp.
CODEN: JKXXAF
DT Patent
LA Japanese
FAN.CNT 1

| | PATENT NO. | KIND | DATE | APPLICATION NO. | DATE |
|------|----------------|------|----------|-----------------|----------|
| | ----- | ---- | ----- | ----- | ----- |
| PI | JP 2003102490 | A2 | 20030408 | JP 2002-214736 | 20020724 |
| | US 2003113899 | A1 | 20030619 | US 2002-196232 | 20020717 |
| | CN 1398964 | A | 20030226 | CN 2002-126904 | 20020725 |
| PRAI | JP 2001-224586 | A | 20010725 | | |

=> d 13 1

L3 ANSWER 1 OF 24 CAPLUS COPYRIGHT 2005 ACS on STN
AN 2004:133959 CAPLUS
DN 140:180654
TI Sulfur-containing animal feed additives from fermentation liquors from microorganisms expressing genes for biosynthesis of sulfur amino acids and derivatives
IN Buchholz, Michael; Binder, Michael; Hermann, Thomas; Pfefferle, Walter; Thierbach, Georg
PA Degussa AG, Germany
SO Eur. Pat. Appl., 22 pp.
CODEN: EPXXDW
DT Patent
LA English
FAN.CNT 1

| | PATENT NO. | KIND | DATE | APPLICATION NO. | DATE |
|------|---|------|----------|------------------|----------|
| | ----- | ---- | ----- | ----- | ----- |
| PI | EP 1389427 | A1 | 20040218 | EP 2003-17146 | 20030729 |
| | R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR, BG, CZ, EE, HU, SK | | | | |
| | DE 10237479 | A1 | 20040226 | DE 2002-10237479 | 20020816 |
| PRAI | DE 2002-10237479 | A | 20020816 | | |

=> d abs 13

L3 ANSWER 1 OF 24 CAPLUS COPYRIGHT 2005 ACS on STN
AB The invention relates to sulfur-containing animal-feed additives such as cysteine, cystine and thiazolidines and their salts produced from fermentation liquors, and to processes for their production The compds. are manufactured by microorganisms expressing genes for enzymes of biosynthesis of these compds. at high levels. Use of a high-level expression construct for the ydeD gene to increase the content of L-cystine and thiazolidines is demonstrated.

=> 13 and (phosphoglycerate or ?serine? or ?cysteine? or ?cystine? or ?glycine) and fermentati?

L3 IS NOT A RECOGNIZED COMMAND

The previous command name entered was not recognized by the system.
For a list of commands available to you in the current file, enter "HELP COMMANDS" at an arrow prompt (=>).

=> d 16 1-3

X
L6 ANSWER 1 OF 3 CAPLUS COPYRIGHT 2005 ACS on STN
AN 2004:133959 CAPLUS
DN 140:180654
TI Sulfur-containing animal feed additives from fermentation
liquors from microorganisms expressing genes for biosynthesis of sulfur
amino acids and derivatives
IN Buchholz, Michael; Binder, Michael; Hermann, Thomas; Pfefferle, Walter;
Thierbach, Georg
PA Degussa AG, Germany
SO Eur. Pat. Appl., 22 pp.
CODEN: EPXXDW
DT Patent
LA English
FAN.CNT 1

| | PATENT NO. | KIND | DATE | APPLICATION NO. | DATE |
|------|--|------|----------|------------------|----------|
| | ----- | ---- | ----- | ----- | ----- |
| PI | EP 1389427 | A1 | 20040218 | EP 2003-17146 | 20030729 |
| | R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR, BG, CZ, EE, HU, SK | | | | |
| | DE 10237479 | A1 | 20040226 | DE 2002-10237479 | 20020816 |
| PRAI | DE 2002-10237479 | A | 20020816 | | |

L6 ANSWER 2 OF 3 CAPLUS COPYRIGHT 2005 ACS on STN
AN 2002:522540 CAPLUS
DN 137:89444
TI Use of ptsH gene of Corynebacterium glutamicum for L-lysine biosynthesis
IN Farwick, Mike; Mockel, Bettina; Pfefferle, Walter
PA Degussa AG, Germany
SO U.S. Pat. Appl. Publ., 15 pp., Cont.-in-part of U.S. Ser. No. 755,187.
CODEN: USXXCO
DT Patent
LA English
FAN.CNT 2

| | PATENT NO. | KIND | DATE | APPLICATION NO. | DATE |
|------|------------------|------|----------|------------------|----------|
| | ----- | ---- | ----- | ----- | ----- |
| PI | US 2002090700 | A1 | 20020711 | US 2001-819930 | 20010329 |
| | US 2003224499 | A9 | 20031204 | | |
| | US 6818432 | B2 | 20041116 | | |
| | DE 10001101 | A1 | 20010719 | DE 2000-10001101 | 20000113 |
| | US 2002094554 | A1 | 20020718 | US 2001-755187 | 20010108 |
| | US 2004005675 | A9 | 20040108 | | |
| | US 2005009143 | A1 | 20050113 | US 2004-916437 | 20040812 |
| PRAI | DE 2000-10001101 | A | 20000113 | | |
| | US 2000-503189 | B2 | 20000214 | | |
| | US 2001-755187 | A2 | 20010108 | | |
| | US 2001-819930 | A3 | 20010329 | | |

L6 ANSWER 3 OF 3 CAPLUS COPYRIGHT 2005 ACS on STN
 AN 2001:867953 CAPLUS
 DN 136:19157
 TI The thrE gene of Corynebacterium glutamicum and its use in increasing
 yields of threonine in fermentation
 IN Rieping, Mechthild
 PA Degussa AG, Germany
 SO Ger. Offen., 24 pp.
 CODEN: GWXXBX
 DT Patent
 LA German
 FAN.CNT 1

| | PATENT NO. | KIND | DATE | APPLICATION NO. | DATE |
|------|---|------|----------|------------------|----------|
| PI | DE 10102823 | A1 | 20011129 | DE 2001-10102823 | 20010123 |
| | CA 2400777 | AA | 20011206 | CA 2001-2400777 | 20010406 |
| | WO 2001092545 | A1 | 20011206 | WO 2001-EP3980 | 20010406 |
| | W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM | | | | |
| | RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG | | | | |
| | EP 1285075 | A1 | 20030226 | EP 2001-931575 | 20010406 |
| | R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR | | | | |
| | US 2002155551 | A1 | 20021024 | US 2001-834721 | 20010416 |
| PRAI | DE 2000-10026494 | A1 | 20000527 | | |
| | US 2000-229328P | P | 20000901 | | |
| | DE 2001-10102823 | A | 20010123 | | |
| | WO 2001-EP3980 | W | 20010406 | | |

SEQUENCE SEARCH SUMMARY

10/620,487

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 3, 2005, 10:50:19 ; Search time 3519 Seconds
(without alignments)
10078.794 Million cell updates/sec

Title: US-10-620-487-1
Perfect score: 750
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
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9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Match | Query Length | DB | ID | Description |
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| 1 | 750 | 100.0 | 750 | 6 | CQ759947 | App/ EPPat 3/04 CQ759947 Sequence |
| 2 | 750 | 100.0 | 10272 | 1 | ECORBAB | Nash 1992? D13169 E.coli gene |
| 3 | 750 | 100.0 | 16446 | 1 | D90886 | Yamamoto 1997 D90886 E.coli geno |

| | | | | | | | | |
|---|----|-------|-------|--------|----|-------------|----------|--------------------|
| | 4 | 750 | 100.0 | 29254 | 1 | ECOK12RIII | Yu 1995 | D64044 Escherichia |
| | 5 | 750 | 100.0 | 110000 | 1 | U00096_27 | 16/2004 | Continuation (28 o |
| | 6 | 745.2 | 99.4 | 12322 | 1 | AE015279 | 2001 Tin | AE015279 Shigella |
| | 7 | 745.2 | 99.4 | 290380 | 1 | AE016987 | | AE016987 Shigella |
| | 8 | 738.8 | 98.5 | 300099 | 1 | AE016764 | | AE016764 Escherich |
| | 9 | 687.6 | 91.7 | 12337 | 1 | AE005488 | | AE005488 Escherich |
| | 10 | 687.6 | 91.7 | 270365 | 1 | AP002562 | | AP002562 Escherich |
| | 11 | 588 | 78.4 | 588 | 6 | E49391 | | E49391 Process for |
| | 12 | 588 | 78.4 | 588 | 6 | AX030083 | | AX030083 Sequence |
| | 13 | 461.2 | 61.5 | 145050 | 1 | AL627275 | | AL627275 Salmonell |
| c | 14 | 461.2 | 61.5 | 300431 | 1 | AE016835 | | AE016835 Salmonell |
| | 15 | 458 | 61.1 | 21722 | 1 | AE008820 | | AE008820 Salmonell |
| | 16 | 265.8 | 35.4 | 618 | 6 | AR388761 | | AR388761 Sequence |
| c | 17 | 224.4 | 29.9 | 23738 | 2 | AC020828 | | AC020828 Mus muscu |
| | 18 | 156 | 20.8 | 372 | 6 | AR388768 | | AR388768 Sequence |
| | 19 | 100 | 13.3 | 100 | 6 | AX999538 | | AX999538 Sequence |
| | 20 | 100 | 13.3 | 100 | 6 | AX999539 | | AX999539 Sequence |
| | 21 | 100 | 13.3 | 100 | 6 | AX999540 | | AX999540 Sequence |
| c | 22 | 70.4 | 9.4 | 288404 | 1 | AE017272 | | AE017272 Bacillus |
| c | 23 | 63.8 | 8.5 | 302451 | 1 | AE016812 | | AE016812 Vibrio vu |
| c | 24 | 55.2 | 7.4 | 110000 | 1 | AE017225_22 | | Continuation (23 o |
| c | 25 | 55.2 | 7.4 | 110000 | 1 | AE017334_22 | | Continuation (23 o |
| c | 26 | 55.2 | 7.4 | 110000 | 1 | AE017355_23 | | Continuation (24 o |
| c | 27 | 55.2 | 7.4 | 293264 | 1 | AE017031 | | AE017031 Bacillus |
| c | 28 | 51 | 6.8 | 249500 | 1 | AP005344 | | AP005344 Vibrio vu |
| | 29 | 50.4 | 6.7 | 573 | 6 | AX432019 | | AX432019 Sequence |
| c | 30 | 49.6 | 6.6 | 300600 | 1 | AP005084 | | AP005084 Vibrio pa |
| c | 31 | 49 | 6.5 | 110000 | 1 | BX950851_45 | | Continuation (46 o |
| | 32 | 48.8 | 6.5 | 344805 | 1 | BX640434 | | BX640434 Bordetell |
| | 33 | 48.8 | 6.5 | 346287 | 1 | BX640450 | | BX640450 Bordetell |
| c | 34 | 47.8 | 6.4 | 304262 | 1 | AE017005 | | AE017005 Bacillus |
| c | 35 | 47.2 | 6.3 | 13848 | 1 | AE004249 | | AE004249 Vibrio ch |
| | 36 | 47.2 | 6.3 | 348171 | 1 | BX640412 | | BX640412 Bordetell |
| c | 37 | 44.4 | 5.9 | 310029 | 1 | AE016868 | | AE016868 Pseudomon |
| c | 38 | 42.8 | 5.7 | 142350 | 5 | BX088596 | | BX088596 Zebrafish |
| c | 39 | 42.8 | 5.7 | 278779 | 2 | BX323579 | | BX323579 Danio rer |
| | 40 | 42 | 5.6 | 669 | 6 | AR319795 | | AR319795 Sequence |
| | 41 | 41.4 | 5.5 | 301214 | 1 | AE016786 | | AE016786 Pseudomon |
| | 42 | 41 | 5.5 | 618 | 12 | AY657639 | | AY657639 Synthetic |
| c | 43 | 41 | 5.5 | 11869 | 1 | AE004657 | | AE004657 Pseudomon |
| c | 44 | 40.6 | 5.4 | 125020 | 9 | AF429315 | | AF429315 Homo sapi |
| | 45 | 40.4 | 5.4 | 14305 | 1 | AE014000 | | AE014000 Yersinia |

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(without alignments)
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Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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12: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Match | Query Length | DB ID | Description |
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| 2 | 588 | 78.4 | 588 | 3 AAA52690 | Aaa52690 Escherich |
| 3 | 295.8 | 39.4 | 1668 | 5 AAS81979 | Aas81979 DNA encod |
| 4 | 265.8 | 35.4 | 618 | 11 ACH99695 | Ach99695 Klebsiell |
| 5 | 156 | 20.8 | 372 | 11 ACH99702 | Ach99702 Klebsiell |

PD 09 4pbt
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WO PID=3/01
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| | 6 | 100 | 13.3 | 100 | 8 | ACD79726 | Acd79726 E. coli K |
| | 7 | 100 | 13.3 | 100 | 8 | ACD79725 | Acd79725 E. coli K |
| | 8 | 100 | 13.3 | 100 | 8 | ACD79727 | Acd79727 E. coli K |
| | 9 | 50.4 | 6.7 | 573 | 6 | ABK73143 | Abk73143 Bacillus |
| | 10 | 42.6 | 5.7 | 2325 | 5 | AAS92926 | Aas92926 DNA encod |
| c | 11 | 42.6 | 5.7 | 3020 | 5 | AAS88917 | Aas88917 DNA encod |
| | 12 | 42 | 5.6 | 669 | 9 | ADA31058 | Ada31058 DNA encod |
| | 13 | 39.8 | 5.3 | 636 | 10 | ADF02251 | Adf02251 Bacterial |
| | 14 | 39.6 | 5.3 | 750 | 11 | ABD10542 | Abd10542 Pseudomon |
| | 15 | 39 | 5.2 | 247682 | 12 | ADL08109 | Adl08109 Human gen |
| | 16 | 38.2 | 5.1 | 636 | 11 | ACH97476 | Ach97476 Klebsiell |
| | 17 | 37.2 | 5.0 | 609 | 10 | ACF70009 | Acf70009 Photorhab |
| c | 18 | 37.2 | 5.0 | 110000 | 10 | ACF65385_1 | Continuation (2 of |
| c | 19 | 37.2 | 5.0 | 110000 | 10 | ACF67367_30 | Continuation (31 o |
| | 20 | 36.4 | 4.9 | 2000 | 8 | ADA71938 | Ada71938 Rice gene |
| c | 21 | 35.6 | 4.7 | 492 | 10 | ACD96860 | Acd96860 Human col |
| | 22 | 35.6 | 4.7 | 612 | 10 | ACF71507 | Acf71507 Photorhab |
| | 23 | 35.6 | 4.7 | 110000 | 10 | ACF67367_46 | Continuation (47 o |
| c | 24 | 35.6 | 4.7 | 110000 | 10 | ACF65388_01 | Continuation (2 of |
| | 25 | 35.2 | 4.7 | 474 | 12 | ADI45188 | Adi45188 Rice isop |
| | 26 | 35.2 | 4.7 | 1302 | 4 | ABL21095 | Abl21095 Drosophil |
| c | 27 | 35.2 | 4.7 | 79467 | 9 | ADA02717 | Ada02717 Mouse Nfa |
| c | 28 | 35.2 | 4.7 | 79467 | 10 | ADB72455 | Adb72455 Mouse Nfa |
| c | 29 | 35.2 | 4.7 | 79467 | 10 | ADE95965 | Ade95965 Mouse Nfa |
| c | 30 | 35 | 4.7 | 1877 | 4 | ABL14601 | Abl14601 Drosophil |
| c | 31 | 35 | 4.7 | 4532 | 4 | ABL14600 | Abl14600 Drosophil |
| c | 32 | 34.6 | 4.6 | 214 | 3 | ADF57362 | Adf57362 Urogenita |
| c | 33 | 34.6 | 4.6 | 3821 | 5 | ADL62643 | Adl62643 Human ova |
| c | 34 | 34.6 | 4.6 | 3825 | 5 | ABV25634 | Abv25634 Human pro |
| c | 35 | 34.4 | 4.6 | 6996 | 4 | ABL21622 | Abl21622 Drosophil |
| | 36 | 34.2 | 4.6 | 592 | 6 | ABT11039 | Abt11039 Human bre |
| | 37 | 34.2 | 4.6 | 645 | 11 | ACH96827 | Ach96827 Klebsiell |
| | 38 | 34.2 | 4.6 | 1707 | 6 | AAS15596 | Aas15596 DNA encod |
| c | 39 | 34.2 | 4.6 | 2000 | 8 | ADA71938 | Ada71938 Rice gene |
| c | 40 | 34.2 | 4.6 | 2000 | 12 | ADJ41214 | Adj41214 Plant cDN |
| | 41 | 33.4 | 4.5 | 202 | 3 | AAC25780 | Aac25780 Human sec |
| c | 42 | 33.4 | 4.5 | 1055 | 3 | AAA07254 | Aaa07254 Asparagin |
| c | 43 | 33.4 | 4.5 | 3077 | 3 | AAA07255 | Aaa07255 Asparagin |
| c | 44 | 33.4 | 4.5 | 9951 | 6 | ABK39929 | Abk39929 Human che |
| | 45 | 33.4 | 4.5 | 29000 | 10 | ADA66458 | Ada66458 Human Tra |

OM nucleic - nucleic search, using sw model

Run on: January 3, 2005, 11:25:37 ; Search time 100 Seconds
 (without alignments)
 5330.917 Million cell updates/sec

Title: US-10-620-487-1
 Perfect score: 750
 Sequence: 1 gatccataaccccaaaccta.....ttagtaacttgctacttaag 750

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Issued_Patents_NA:*
 1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
 2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
 5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
 6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result | | % | | | | | |
|--------|-------|-------------|--------|----|----------------------|-------------|-------------------|
| No. | Score | Query Match | Length | DB | ID | Description | |
| 1 | 265.8 | 35.4 | 618 | 4 | US-09-489-039A-5490 | X | Sequence 5490, Ap |
| 2 | 156 | 20.8 | 372 | 4 | US-09-489-039A-5497 | | Sequence 5497, Ap |
| 3 | 42 | 5.6 | 669 | 4 | US-09-328-352-2345 | | Sequence 2345, Ap |
| 4 | 39.8 | 5.3 | 636 | 4 | US-09-543-681A-2536 | | Sequence 2536, Ap |
| 5 | 39.6 | 5.3 | 750 | 4 | US-09-252-991A-9146 | | Sequence 9146, Ap |
| 6 | 38.2 | 5.1 | 636 | 4 | US-09-489-039A-3271 | | Sequence 3271, Ap |
| 7 | 34.2 | 4.6 | 645 | 4 | US-09-489-039A-2622 | | Sequence 2622, Ap |
| 8 | 33.4 | 4.5 | 202 | 4 | US-09-513-999C-29855 | | Sequence 29855, A |
| c 9 | 33.4 | 4.5 | 1055 | 3 | US-09-410-028-1 | | Sequence 1, Appli |
| c 10 | 33.4 | 4.5 | 3077 | 3 | US-09-410-028-3 | | Sequence 3, Appli |
| 11 | 33 | 4.4 | 72604 | 3 | US-09-268-992-7 | | Sequence 7, Appli |

| | | | | | | | |
|---|----|------|-----|---------|---|----------------------|-------------------|
| | 12 | 33 | 4.4 | 72604 | 3 | US-09-657-474-7 | Sequence 7, Appli |
| c | 13 | 32.8 | 4.4 | 1194 | 4 | US-09-252-991A-9124 | Sequence 9124, Ap |
| c | 14 | 32.8 | 4.4 | 1326 | 4 | US-09-252-991A-9206 | Sequence 9206, Ap |
| | 15 | 32.8 | 4.4 | 1329 | 4 | US-09-252-991A-8853 | Sequence 8853, Ap |
| | 16 | 32.6 | 4.3 | 505 | 4 | US-09-621-976-15639 | Sequence 15639, A |
| c | 17 | 32.2 | 4.3 | 1001 | 4 | US-09-641-638-340 | Sequence 340, App |
| c | 18 | 32.2 | 4.3 | 1001 | 4 | US-10-170-097-340 | Sequence 340, App |
| | 19 | 32.2 | 4.3 | 5127 | 4 | US-09-462-606-1 | Sequence 1, Appli |
| | 20 | 32.2 | 4.3 | 7207 | 4 | US-09-462-606-3 | Sequence 3, Appli |
| c | 21 | 32 | 4.3 | 1338 | 4 | US-09-489-039A-6698 | Sequence 6698, Ap |
| c | 22 | 31.8 | 4.2 | 789 | 4 | US-09-134-000C-2827 | Sequence 2827, Ap |
| c | 23 | 31.4 | 4.2 | 965 | 4 | US-09-270-767-14185 | Sequence 14185, A |
| | 24 | 31.2 | 4.2 | 1230025 | 4 | US-09-198-452A-1 | Sequence 1, Appli |
| | 25 | 30.8 | 4.1 | 726 | 4 | US-09-328-352-3033 | Sequence 3033, Ap |
| c | 26 | 30.8 | 4.1 | 936 | 4 | US-09-489-039A-5469 | Sequence 5469, Ap |
| | 27 | 30.8 | 4.1 | 1040 | 4 | US-09-602-787A-305 | Sequence 305, App |
| c | 28 | 30.8 | 4.1 | 1497 | 4 | US-09-220-132-94 | Sequence 94, Appl |
| | 29 | 30.8 | 4.1 | 1500 | 4 | US-09-602-787A-301 | Sequence 301, App |
| | 30 | 30.6 | 4.1 | 1269 | 4 | US-09-489-039A-3734 | Sequence 3734, Ap |
| | 31 | 30.6 | 4.1 | 5396 | 4 | US-09-270-767-29115 | Sequence 29115, A |
| | 32 | 30.6 | 4.1 | 7233 | 4 | US-09-270-767-13200 | Sequence 13200, A |
| c | 33 | 30.4 | 4.1 | 1294 | 2 | US-08-665-647-4 | Sequence 4, Appli |
| c | 34 | 30.4 | 4.1 | 1521 | 4 | US-09-252-991A-6495 | Sequence 6495, Ap |
| c | 35 | 30.4 | 4.1 | 4599 | 4 | US-09-302-626B-61 | Sequence 61, Appl |
| c | 36 | 30.4 | 4.1 | 5562 | 4 | US-10-204-708-63 | Sequence 63, Appl |
| | 37 | 30.4 | 4.1 | 9018 | 4 | US-10-220-587-3 | Sequence 3, Appli |
| | 38 | 30.2 | 4.0 | 636 | 4 | US-09-489-039A-2437 | Sequence 2437, Ap |
| c | 39 | 30.2 | 4.0 | 854 | 4 | US-09-302-626B-57 | Sequence 57, Appl |
| c | 40 | 30.2 | 4.0 | 5937 | 4 | US-09-302-626B-59 | Sequence 59, Appl |
| c | 41 | 30.2 | 4.0 | 38564 | 4 | US-09-734-673-3 | Sequence 3, Appli |
| c | 42 | 30 | 4.0 | 454 | 4 | US-09-513-999C-10704 | Sequence 10704, A |
| | 43 | 30 | 4.0 | 832 | 4 | US-09-621-976-2813 | Sequence 2813, Ap |
| c | 44 | 30 | 4.0 | 849 | 4 | US-09-540-236-656 | Sequence 656, App |
| | 45 | 30 | 4.0 | 1173 | 4 | US-09-248-796A-6337 | Sequence 6337, Ap |

OM nucleic - nucleic search, using sw model

Run on: January 3, 2005, 10:05:31 ; Search time 520 Seconds
(without alignments)
8146.523 Million cell updates/sec

Title: US-10-620-487-1
Perfect score: 750
Sequence: 1 gatccataaccccaaaccta.....ttagtaacttgctacttaag 750

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4176236 seqs, 2824127955 residues

Total number of hits satisfying chosen parameters: 8352472

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
- 17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
- 18: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 19: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
- 20: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 21: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result | % | | | | | Description |
|--------|-----|-------|--------------------|---------|----|--|
| | No. | Score | Query Match Length | DB | ID | |
| | 1 | 750 | 100.0 | 750 | 16 | US-10-620-487-1 <i>App 1</i> Sequence 1, Appli |
| | 2 | 50.4 | 6.7 | 573 | 9 | US-09-974-300-434 Sequence 434, App |
| | 3 | 39 | 5.2 | 247682 | 16 | US-10-235-192A-28 Sequence 28, Appl |
| | 4 | 36.8 | 4.9 | 852 | 16 | US-10-425-114-35996 Sequence 35996, A |
| | 5 | 36.8 | 4.9 | 2727 | 18 | US-10-425-115-65647 Sequence 65647, A |
| c | 6 | 36 | 4.8 | 486 | 17 | US-10-767-795-2906 Sequence 2906, Ap |
| | 7 | 35.2 | 4.7 | 474 | 16 | US-10-259-194A-119 Sequence 119, App |
| c | 8 | 35.2 | 4.7 | 79467 | 16 | US-10-052-482-223 Sequence 223, App |
| c | 9 | 34.6 | 4.6 | 214 | 9 | US-09-933-797-681 Sequence 681, App |
| c | 10 | 34.6 | 4.6 | 3821 | 10 | US-09-814-353-20855 Sequence 20855, A |
| c | 11 | 34.6 | 4.6 | 3825 | 18 | US-10-357-930-25623 Sequence 25623, A |
| c | 12 | 34.4 | 4.6 | 6630 | 17 | US-10-437-963-75212 Sequence 75212, A |
| c | 13 | 34.2 | 4.6 | 2000 | 16 | US-10-260-238-2214 Sequence 2214, Ap |
| c | 14 | 34.2 | 4.6 | 141463 | 13 | US-10-087-192-22 Sequence 22, Appl |
| c | 15 | 33.8 | 4.5 | 497 | 16 | US-10-424-599-84060 Sequence 84060, A |
| c | 16 | 33.4 | 4.5 | 2924 | 16 | US-10-424-599-28594 Sequence 28594, A |
| c | 17 | 33.4 | 4.5 | 9951 | 16 | US-10-257-166-10 Sequence 10, Appl |
| | 18 | 33.4 | 4.5 | 29000 | 10 | US-09-906-158-17 Sequence 17, Appl |
| | 19 | 33.4 | 4.5 | 29000 | 15 | US-10-388-263-466 Sequence 466, App |
| | 20 | 33.2 | 4.4 | 235 | 16 | US-10-424-599-141309 Sequence 141309, |
| | 21 | 33.2 | 4.4 | 826 | 16 | US-10-424-599-97789 Sequence 97789, A |
| | 22 | 33.2 | 4.4 | 3673778 | 15 | US-10-312-841-2 Sequence 2, Appli |
| | 23 | 33 | 4.4 | 72604 | 15 | US-10-162-497-7 Sequence 7, Appli |
| | 24 | 33 | 4.4 | 72604 | 17 | US-10-629-313-7 Sequence 7, Appli |
| | 25 | 32.8 | 4.4 | 64492 | 16 | US-10-378-083-1 Sequence 1, Appli |
| | 26 | 32.6 | 4.3 | 451 | 14 | US-10-123-155-126 Sequence 126, App |
| | 27 | 32.6 | 4.3 | 451 | 15 | US-10-146-731-126 Sequence 126, App |
| | 28 | 32.6 | 4.3 | 451 | 15 | US-10-140-472-126 Sequence 126, App |
| | 29 | 32.6 | 4.3 | 451 | 15 | US-10-141-761-126 Sequence 126, App |
| | 30 | 32.6 | 4.3 | 451 | 15 | US-10-142-885-126 Sequence 126, App |
| | 31 | 32.6 | 4.3 | 451 | 15 | US-10-158-790-126 Sequence 126, App |
| | 32 | 32.6 | 4.3 | 451 | 15 | US-10-137-871-126 Sequence 126, App |
| | 33 | 32.6 | 4.3 | 451 | 15 | US-10-140-923-126 Sequence 126, App |
| | 34 | 32.6 | 4.3 | 451 | 15 | US-10-141-756-126 Sequence 126, App |
| | 35 | 32.6 | 4.3 | 451 | 15 | US-10-141-759-126 Sequence 126, App |
| | 36 | 32.6 | 4.3 | 451 | 15 | US-10-140-805-126 Sequence 126, App |
| | 37 | 32.6 | 4.3 | 451 | 15 | US-10-140-864-126 Sequence 126, App |
| | 38 | 32.6 | 4.3 | 451 | 16 | US-10-142-426-126 Sequence 126, App |
| | 39 | 32.6 | 4.3 | 597 | 18 | US-10-363-345A-13041 Sequence 13041, A |
| c | 40 | 32.6 | 4.3 | 597 | 18 | US-10-363-345A-13042 Sequence 13042, A |
| c | 41 | 32.6 | 4.3 | 623 | 17 | US-10-767-701-883 Sequence 883, App |
| | 42 | 32.6 | 4.3 | 858 | 18 | US-10-363-345A-21325 Sequence 21325, A |
| c | 43 | 32.6 | 4.3 | 858 | 18 | US-10-363-345A-21326 Sequence 21326, A |
| c | 44 | 32.6 | 4.3 | 2589 | 18 | US-10-425-115-175990 Sequence 175990, |
| c | 45 | 32.4 | 4.3 | 289 | 17 | US-10-437-963-54974 Sequence 54974, A |

OM nucleic - nucleic search, using sw model

Run on: January 3, 2005, 11:23:52 ; Search time 3085 Seconds
(without alignments)
8858.930 Million cell updates/sec

Title: US-10-620-487-1
Perfect score: 750
Sequence: 1 gatccataaccccaaaccta.....ttagtaacttgctacttaag 750

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result | No. | Score | % Match | Query Length | DB ID | Description |
|--------|-----|-------|---------|--------------|-------|--------------------|
| c | 1 | 473 | 63.1 | 681 | 6 | CA366654 642278 NC |
| | 2 | 351 | 46.8 | 856 | 9 | CL650636 PRI0110a_ |
| | 3 | 331.4 | 44.2 | 791 | 9 | CL688782 PRI014b_G |
| | 4 | 321.6 | 42.9 | 736 | 9 | CL688905 PRI014d_C |
| c | 5 | 113.2 | 15.1 | 118 | 6 | CA374430 648800 NC |
| c | 6 | 55.2 | 7.4 | 819 | 8 | BH447440 BOHQB49TF |
| | 7 | 50 | 6.7 | 420 | 8 | BH374397 AG-ND-180 |
| c | 8 | 49.4 | 6.6 | 862 | 9 | CL666889 PRI0153c_ |

| | | | | | | | | |
|---|----|------|-----|------|---|----------|----------|-----------|
| | 9 | 43.4 | 5.8 | 450 | 8 | BH379453 | BH379453 | AG-ND-163 |
| c | 10 | 39.2 | 5.2 | 938 | 9 | CL139330 | CL139330 | ISB1-112E |
| c | 11 | 38.2 | 5.1 | 474 | 9 | AG240288 | AG240288 | Lotus cor |
| | 12 | 38.2 | 5.1 | 1101 | 9 | CNS00EEC | AL069085 | Drosophil |
| c | 13 | 37.6 | 5.0 | 553 | 5 | BM965274 | BM965274 | kj93h10.y |
| c | 14 | 37.6 | 5.0 | 568 | 5 | BQ095448 | BQ095448 | kk05d05.y |
| c | 15 | 37.6 | 5.0 | 583 | 5 | BM965121 | BM965121 | kj92c03.y |
| c | 16 | 37.6 | 5.0 | 623 | 5 | BM965443 | BM965443 | kj95h06.y |
| c | 17 | 37.6 | 5.0 | 637 | 5 | BM965333 | BM965333 | kj94f01.y |
| c | 18 | 37.4 | 5.0 | 493 | 9 | CE114952 | CE114952 | tigr-gss- |
| | 19 | 37.4 | 5.0 | 884 | 9 | CNS006U0 | AL065923 | Drosophil |
| c | 20 | 37.2 | 5.0 | 939 | 9 | CNS00CNG | AL059400 | Drosophil |
| | 21 | 36.8 | 4.9 | 614 | 5 | BQ628514 | BQ628514 | sap47h10. |
| | 22 | 36.8 | 4.9 | 650 | 6 | CD598566 | CD598566 | RK114A3B1 |
| | 23 | 36.8 | 4.9 | 650 | 6 | CD599088 | CD599088 | RK114A4B0 |
| c | 24 | 36.8 | 4.9 | 712 | 9 | BX163185 | BX163185 | Danio rer |
| | 25 | 36.8 | 4.9 | 778 | 9 | BX175544 | BX175544 | Danio rer |
| | 26 | 36.6 | 4.9 | 408 | 8 | BZ716786 | BZ716786 | OGEBE26TM |
| | 27 | 36.6 | 4.9 | 589 | 9 | CC604749 | CC604749 | OGUHO32TH |
| c | 28 | 36.6 | 4.9 | 787 | 9 | CNS016H3 | AL106737 | Drosophil |
| c | 29 | 36.6 | 4.9 | 935 | 9 | CC604756 | CC604756 | OGUHO32TV |
| | 30 | 36.6 | 4.9 | 963 | 9 | CG050339 | CG050339 | PUIIH51TB |
| | 31 | 36.4 | 4.9 | 440 | 6 | CA678514 | CA678514 | wlm12.pk0 |
| c | 32 | 36.4 | 4.9 | 566 | 6 | CD347163 | CD347163 | EtESTef11 |
| c | 33 | 36.4 | 4.9 | 619 | 5 | BM964489 | BM964489 | kj84e08.y |
| | 34 | 36.2 | 4.8 | 825 | 9 | CC534336 | CC534336 | CH240_412 |
| c | 35 | 36 | 4.8 | 630 | 5 | BM964821 | BM964821 | kj88g02.y |
| c | 36 | 36 | 4.8 | 688 | 8 | BZ659718 | BZ659718 | OGCCC31TM |
| c | 37 | 35.8 | 4.8 | 1181 | 9 | AG127050 | AG127050 | Pan trogl |
| c | 38 | 35.6 | 4.7 | 492 | 1 | AI908572 | AI908572 | RC-BT177- |
| c | 39 | 35.4 | 4.7 | 699 | 9 | CE799079 | CE799079 | tigr-gss- |
| | 40 | 35.4 | 4.7 | 733 | 8 | BZ389118 | BZ389118 | EINDJ32TF |
| | 41 | 35.4 | 4.7 | 792 | 9 | CG872981 | CG872981 | ZMMBBc028 |
| c | 42 | 35.2 | 4.7 | 226 | 4 | BG370992 | BG370992 | dac11a02. |
| | 43 | 35.2 | 4.7 | 500 | 5 | BP188868 | BP188868 | BP188868 |
| | 44 | 35.2 | 4.7 | 500 | 5 | BP189161 | BP189161 | BP189161 |
| c | 45 | 35.2 | 4.7 | 552 | 9 | BX163834 | BX163834 | Danio rer |

P

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 3, 2005, 07:57:25 ; Search time 81 Seconds
(without alignments)
863.608 Million cell updates/sec

Title: US-10-620-487-2
Perfect score: 996
Sequence: 1 VTPTLLSAFWTYTLITAMTP.....RQLNIVLALLLVYCAVRIFY 195

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID | Description |
|------------|-------|-------------|--------|----|----------|--------------------|
| 1 | 996 | 100.0 | 195 | 8 | ADK66006 | Adk66006 E coli Yf |
| 2 | 993 | 99.7 | 195 | 3 | AAB01788 | Aab01788 Escherich |
| 3 | 684 | 68.7 | 205 | 7 | ABO66144 | Abo66144 Klebsiell |
| 4 | 505 | 50.7 | 344 | 4 | ABG17792 | Abg17792 Novel hum |
| 5 | 272.5 | 27.4 | 249 | 7 | ABO76971 | Abo76971 Pseudomon |
| 6 | 256 | 25.7 | 203 | 6 | ABM70439 | Abm70439 Photorhab |
| 7 | 250.5 | 25.2 | 211 | 7 | ABO63925 | Abo63925 Klebsiell |
| 8 | 232.5 | 23.3 | 212 | 7 | ADF04482 | Adf04482 Bacterial |
| 9 | 228.5 | 22.9 | 211 | 7 | ADF06423 | Adf06423 Bacterial |

| | | | | | | | |
|----|-------|------|-----|---|----------|----------|-----------|
| 10 | 191.5 | 19.2 | 238 | 6 | ADA35835 | Ada35835 | Acinetoba |
| 11 | 178 | 17.9 | 241 | 6 | ADA35872 | Ada35872 | Acinetoba |
| 12 | 173 | 17.4 | 271 | 7 | ABO83709 | Abo83709 | Pseudomon |
| 13 | 163.5 | 16.4 | 235 | 6 | ADA36962 | Ada36962 | Acinetoba |
| 14 | 162 | 16.3 | 214 | 7 | ABO61549 | Abo61549 | Klebsiell |
| 15 | 161.5 | 16.2 | 206 | 6 | ABU32233 | Abu32233 | Protein e |
| 16 | 158.5 | 15.9 | 206 | 7 | ABO70000 | Abo70000 | Pseudomon |
| 17 | 158.5 | 15.9 | 211 | 6 | ABU39959 | Abu39959 | Protein e |
| 18 | 157.5 | 15.8 | 190 | 4 | ABG29208 | Abg29208 | Novel hum |
| 19 | 157.5 | 15.8 | 206 | 6 | ABU28287 | Abu28287 | Protein e |
| 20 | 156.5 | 15.7 | 206 | 6 | ABU50100 | Abu50100 | Protein e |
| 21 | 156.5 | 15.7 | 206 | 6 | ABU47858 | Abu47858 | Protein e |
| 22 | 155.5 | 15.6 | 214 | 6 | ADA34738 | Ada34738 | Acinetoba |
| 23 | 155.5 | 15.6 | 237 | 7 | ABO78429 | Abo78429 | Pseudomon |
| 24 | 154 | 15.5 | 205 | 6 | ABU44939 | Abu44939 | Protein e |
| 25 | 154 | 15.5 | 210 | 6 | ADA35521 | Ada35521 | Acinetoba |
| 26 | 153.5 | 15.4 | 211 | 7 | ABO72001 | Abo72001 | Pseudomon |
| 27 | 153 | 15.4 | 214 | 7 | ABO63276 | Abo63276 | Klebsiell |
| 28 | 151.5 | 15.2 | 211 | 6 | ABU19902 | Abu19902 | Protein e |
| 29 | 149.5 | 15.0 | 250 | 7 | ADF04202 | Adf04202 | Bacterial |
| 30 | 148 | 14.9 | 211 | 7 | ABO63091 | Abo63091 | Klebsiell |
| 31 | 146.5 | 14.7 | 220 | 6 | ADA33616 | Ada33616 | Acinetoba |
| 32 | 146 | 14.7 | 222 | 6 | ADA35184 | Ada35184 | Acinetoba |
| 33 | 143.5 | 14.4 | 212 | 3 | AAB01787 | Aab01787 | Escherich |
| 34 | 138.5 | 13.9 | 219 | 7 | ABO61214 | Abo61214 | Klebsiell |
| 35 | 137.5 | 13.8 | 205 | 6 | ABU49040 | Abu49040 | Protein e |
| 36 | 132 | 13.3 | 208 | 6 | ADA33824 | Ada33824 | Acinetoba |
| 37 | 129 | 13.0 | 201 | 6 | ABM68999 | Abm68999 | Photorhab |
| 38 | 128.5 | 12.9 | 228 | 7 | ADF04569 | Adf04569 | Bacterial |
| 39 | 128.5 | 12.9 | 240 | 6 | ADA36250 | Ada36250 | Acinetoba |
| 40 | 128 | 12.9 | 220 | 7 | ADF04260 | Adf04260 | Bacterial |
| 41 | 127 | 12.8 | 200 | 6 | ADA33486 | Ada33486 | Acinetoba |
| 42 | 126 | 12.7 | 205 | 3 | AAY79298 | Aay79298 | E. coli R |
| 43 | 126 | 12.7 | 205 | 3 | AAY99597 | Aay99597 | E. coli L |
| 44 | 125.5 | 12.6 | 214 | 6 | ADA35408 | Ada35408 | Acinetoba |
| 45 | 123.5 | 12.4 | 209 | 6 | ABU38890 | Abu38890 | Protein e |

OM protein - protein search, using sw model

Run on: January 3, 2005, 08:54:35 ; Search time 25 Seconds
 (without alignments)
 517.280 Million cell updates/sec

Title: US-10-620-487-2
 Perfect score: 996
 Sequence: 1 VTPTLLSAFWTYTLITAMTP.....RQLNIVLALLLVYCAVRIFY 195

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Issued_Patents_AA:*
 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
 5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Match | Query Length | DB | ID | Description |
|------------|-------|---------|--------------|----|----------------------|-------------------|
| 1 | 684 | 68.7 | 205 | 4 | US-09-489-039A-12661 | Sequence 12661, A |
| 2 | 272.5 | 27.4 | 249 | 4 | US-09-252-991A-25717 | Sequence 25717, A |
| 3 | 250.5 | 25.2 | 211 | 4 | US-09-489-039A-10442 | Sequence 10442, A |
| 4 | 232.5 | 23.3 | 212 | 4 | US-09-543-681A-4767 | Sequence 4767, Ap |
| 5 | 228.5 | 22.9 | 211 | 4 | US-09-543-681A-6708 | Sequence 6708, Ap |
| 6 | 191.5 | 19.2 | 238 | 4 | US-09-328-352-7122 | Sequence 7122, Ap |
| 7 | 178 | 17.9 | 241 | 4 | US-09-328-352-7159 | Sequence 7159, Ap |
| 8 | 173 | 17.4 | 271 | 4 | US-09-252-991A-32455 | Sequence 32455, A |
| 9 | 163.5 | 16.4 | 235 | 4 | US-09-328-352-8249 | Sequence 8249, Ap |
| 10 | 162 | 16.3 | 214 | 4 | US-09-489-039A-8066 | Sequence 8066, Ap |
| 11 | 158.5 | 15.9 | 206 | 4 | US-09-252-991A-18746 | Sequence 18746, A |

| | | | | | | |
|----|-------|------|-----|---|----------------------|-------------------|
| 12 | 155.5 | 15.6 | 214 | 4 | US-09-328-352-6025 | Sequence 6025, Ap |
| 13 | 155.5 | 15.6 | 237 | 4 | US-09-252-991A-27175 | Sequence 27175, A |
| 14 | 154 | 15.5 | 210 | 4 | US-09-328-352-6808 | Sequence 6808, Ap |
| 15 | 153.5 | 15.4 | 211 | 4 | US-09-252-991A-20747 | Sequence 20747, A |
| 16 | 153 | 15.4 | 214 | 4 | US-09-489-039A-9793 | Sequence 9793, Ap |
| 17 | 149.5 | 15.0 | 250 | 4 | US-09-543-681A-4487 | Sequence 4487, Ap |
| 18 | 148 | 14.9 | 211 | 4 | US-09-489-039A-9608 | Sequence 9608, Ap |
| 19 | 146.5 | 14.7 | 220 | 4 | US-09-328-352-4903 | Sequence 4903, Ap |
| 20 | 146 | 14.7 | 222 | 4 | US-09-328-352-6471 | Sequence 6471, Ap |
| 21 | 138.5 | 13.9 | 219 | 4 | US-09-489-039A-7731 | Sequence 7731, Ap |
| 22 | 132 | 13.3 | 208 | 4 | US-09-328-352-5111 | Sequence 5111, Ap |
| 23 | 128.5 | 12.9 | 228 | 4 | US-09-543-681A-4854 | Sequence 4854, Ap |
| 24 | 128.5 | 12.9 | 240 | 4 | US-09-328-352-7537 | Sequence 7537, Ap |
| 25 | 128 | 12.9 | 220 | 4 | US-09-543-681A-4545 | Sequence 4545, Ap |
| 26 | 127 | 12.8 | 200 | 4 | US-09-328-352-4773 | Sequence 4773, Ap |
| 27 | 126 | 12.7 | 205 | 3 | US-09-396-357-2 | Sequence 2, Appli |
| 28 | 125.5 | 12.6 | 214 | 4 | US-09-328-352-6695 | Sequence 6695, Ap |
| 29 | 123.5 | 12.4 | 228 | 4 | US-09-252-991A-23837 | Sequence 23837, A |
| 30 | 123.5 | 12.4 | 277 | 4 | US-09-252-991A-23018 | Sequence 23018, A |
| 31 | 122.5 | 12.3 | 201 | 4 | US-09-328-352-6409 | Sequence 6409, Ap |
| 32 | 115.5 | 11.6 | 260 | 4 | US-09-252-991A-25992 | Sequence 25992, A |
| 33 | 112.5 | 11.3 | 249 | 4 | US-09-328-352-5813 | Sequence 5813, Ap |
| 34 | 112 | 11.2 | 217 | 4 | US-09-489-039A-8076 | Sequence 8076, Ap |
| 35 | 111.5 | 11.2 | 222 | 4 | US-09-252-991A-26644 | Sequence 26644, A |
| 36 | 109.5 | 11.0 | 216 | 4 | US-09-252-991A-18666 | Sequence 18666, A |
| 37 | 107.5 | 10.8 | 206 | 4 | US-09-328-352-4784 | Sequence 4784, Ap |
| 38 | 105.5 | 10.6 | 209 | 4 | US-09-328-352-8225 | Sequence 8225, Ap |
| 39 | 104.5 | 10.5 | 210 | 4 | US-09-328-352-4775 | Sequence 4775, Ap |
| 40 | 103.5 | 10.4 | 226 | 4 | US-09-252-991A-31610 | Sequence 31610, A |
| 41 | 102.5 | 10.3 | 221 | 4 | US-09-328-352-6659 | Sequence 6659, Ap |
| 42 | 99 | 9.9 | 213 | 4 | US-09-489-039A-11845 | Sequence 11845, A |
| 43 | 98.5 | 9.9 | 138 | 4 | US-09-711-164-445 | Sequence 445, App |
| 44 | 98.5 | 9.9 | 269 | 4 | US-09-489-039A-7320 | Sequence 7320, Ap |
| 45 | 97.5 | 9.8 | 450 | 4 | US-09-252-991A-20484 | Sequence 20484, A |

OM protein - protein search, using sw model

Run on: January 3, 2005, 08:41:11 ; Search time 444 Seconds
(without alignments)
157.989 Million cell updates/sec

Title: US-10-620-487-2
Perfect score: 996
Sequence: 1 VTPTLLSAFWTYTLITAMTP.....RQLNIVLALLLVYCAVRIFY 195

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1599051 seqs, 359727711 residues

Total number of hits satisfying chosen parameters: 1599051

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep:*
- 17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
- 19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
- 20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID | Description |
|---------------|-------|----------------|--------|----|----------------------------|-------------------|
| 1 | 996 | 100.0 | 195 | 15 | US-10-620-487-2 <i>low</i> | Sequence 2, Appli |
| 2 | 161.5 | 16.2 | 206 | 15 | US-10-282-122A-60157 | Sequence 60157, A |
| 3 | 158.5 | 15.9 | 211 | 15 | US-10-282-122A-67883 | Sequence 67883, A |
| 4 | 157.5 | 15.8 | 206 | 15 | US-10-282-122A-56211 | Sequence 56211, A |
| 5 | 156.5 | 15.7 | 206 | 15 | US-10-282-122A-75782 | Sequence 75782, A |
| 6 | 156.5 | 15.7 | 206 | 15 | US-10-282-122A-78024 | Sequence 78024, A |
| 7 | 154 | 15.5 | 205 | 15 | US-10-282-122A-72863 | Sequence 72863, A |
| 8 | 151.5 | 15.2 | 211 | 15 | US-10-282-122A-47826 | Sequence 47826, A |
| 9 | 142 | 14.3 | 217 | 14 | US-10-156-761-10918 | Sequence 10918, A |
| 10 | 137.5 | 13.8 | 205 | 15 | US-10-282-122A-76964 | Sequence 76964, A |
| 11 | 126 | 12.7 | 205 | 9 | US-09-927-395-2 | Sequence 2, Appli |
| 12 | 126 | 12.7 | 205 | 9 | US-09-847-392-2 | Sequence 2, Appli |
| 13 | 123.5 | 12.4 | 209 | 15 | US-10-282-122A-66814 | Sequence 66814, A |
| 14 | 120 | 12.0 | 181 | 15 | US-10-282-122A-44873 | Sequence 44873, A |
| 15 | 117.5 | 11.8 | 210 | 15 | US-10-282-122A-69338 | Sequence 69338, A |
| 16 | 116.5 | 11.7 | 223 | 9 | US-09-738-626-6070 | Sequence 6070, Ap |
| 17 | 116.5 | 11.7 | 223 | 10 | US-09-746-660A-14 | Sequence 14, Appl |
| 18 | 112 | 11.2 | 207 | 9 | US-09-738-626-6418 | Sequence 6418, Ap |
| 19 | 112 | 11.2 | 227 | 15 | US-10-461-194-124 | Sequence 124, App |
| 20 | 111 | 11.1 | 227 | 15 | US-10-461-194-94 | Sequence 94, Appl |
| 21 | 110.5 | 11.1 | 205 | 14 | US-10-156-761-11297 | Sequence 11297, A |
| 22 | 109.5 | 11.0 | 209 | 15 | US-10-282-122A-51102 | Sequence 51102, A |
| 23 | 107.5 | 10.8 | 224 | 14 | US-10-156-761-7796 | Sequence 7796, Ap |
| 24 | 104 | 10.4 | 226 | 9 | US-09-738-626-3665 | Sequence 3665, Ap |
| 25 | 98.5 | 9.9 | 138 | 14 | US-10-287-274-445 | Sequence 445, App |
| 26 | 98.5 | 9.9 | 138 | 15 | US-10-282-122A-42680 | Sequence 42680, A |
| 27 | 96 | 9.6 | 948 | 16 | US-10-437-963-161288 | Sequence 161288, |
| 28 | 95.5 | 9.6 | 473 | 15 | US-10-282-122A-61289 | Sequence 61289, A |
| 29 | 95 | 9.5 | 537 | 15 | US-10-282-122A-68111 | Sequence 68111, A |
| 30 | 93.5 | 9.4 | 212 | 15 | US-10-374-903A-6 | Sequence 6, Appli |
| 31 | 92 | 9.2 | 486 | 14 | US-10-369-493-15301 | Sequence 15301, A |
| 32 | 92 | 9.2 | 488 | 14 | US-10-369-493-15667 | Sequence 15667, A |
| 33 | 92 | 9.2 | 488 | 14 | US-10-369-493-16057 | Sequence 16057, A |
| 34 | 92 | 9.2 | 625 | 14 | US-10-369-493-3850 | Sequence 3850, Ap |
| 35 | 91.5 | 9.2 | 264 | 11 | US-09-864-408A-4810 | Sequence 4810, Ap |
| 36 | 91 | 9.1 | 246 | 15 | US-10-424-599-253409 | Sequence 253409, |
| 37 | 91 | 9.1 | 470 | 16 | US-10-767-701-44234 | Sequence 44234, A |
| 38 | 91 | 9.1 | 551 | 9 | US-09-738-626-4431 | Sequence 4431, Ap |
| 39 | 91 | 9.1 | 551 | 15 | US-10-627-476-510 | Sequence 510, App |
| 40 | 90.5 | 9.1 | 680 | 16 | US-10-437-963-142247 | Sequence 142247, |
| 41 | 90 | 9.0 | 204 | 14 | US-10-156-761-8429 | Sequence 8429, Ap |
| 42 | 90 | 9.0 | 468 | 15 | US-10-282-122A-52688 | Sequence 52688, A |
| 43 | 90 | 9.0 | 552 | 15 | US-10-282-122A-53662 | Sequence 53662, A |
| 44 | 89.5 | 9.0 | 754 | 15 | US-10-282-122A-48878 | Sequence 48878, A |
| 45 | 88.5 | 8.9 | 536 | 11 | US-09-809-665A-71 | Sequence 71, Appl |

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OM protein - nucleic search, using frame_plus_p2n model

Run on: January 3, 2005, 09:05:56 ; Search time 4048 Seconds
(without alignments)
2278.036 Million cell updates/sec

Title: US-10-620-487-2
Perfect score: 996
Sequence: 1 VTPTLLSAFWTYTLITAMTP.....RQLNIVLALLLVYCAVRIFY 195

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlh

Q=/cgn2_1/USPTO_spool/US10620487/runat_29122004_134449_9000/app_query.fasta_1.39
1

-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10620487_@CGN_1_1_3731_@runat_29122004_134449_9000 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*

11: gb_sts:*
 12: gb_sy:*
 13: gb_un:*
 14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|------------|-------|---------------|--------|----|--------------------------|----------------------|
| 1 | 996 | 100.0 | 588 | 6 | E49391 JP 7/00 | E49391 Process for ★ |
| 2 | 996 | 100.0 | 588 | 6 | AX030083 Livshits 7/00 | AX030083 Sequence |
| 3 | 996 | 100.0 | 750 | 6 | CQ759947 Appl | CQ759947 Sequence |
| 4 | 996 | 100.0 | 10272 | 1 | ECORBAB X | D13169 E.coli gene |
| 5 | 996 | 100.0 | 16446 | 1 | D90886 SEQ 1997 Yamanaka | D90886 E.coli geno |
| 6 | 996 | 100.0 | 29254 | 1 | ECOK12RIII SEB 1985 X | D64044 Escherichia |
| 7 | 996 | 100.0 | 110000 | 1 | U00096 27 SEQ X | Continuation (28 o |
| 8 | 992 | 99.6 | 300099 | 1 | AE016764 X " | AE016764 Escherich |
| 9 | 990 | 99.4 | 12322 | 1 | AE015279 X " | AE015279 Shigella |
| 10 | 990 | 99.4 | 290380 | 1 | AE016987 X " | AE016987 Shigella |
| 11 | 982 | 98.6 | 12337 | 1 | AE005488 X " | AE005488 Escherich |
| 12 | 982 | 98.6 | 270365 | 1 | AP002562 X " | AP002562 Escherich |
| 13 | 887 | 89.1 | 21722 | 1 | AE008820 Y | AE008820 Salmonell |
| 14 | 887 | 89.1 | 145050 | 1 | AL627275 Y | AL627275 Salmonell |
| c 15 | 887 | 89.1 | 300431 | 1 | AE016835 | AE016835 Salmonell |
| 16 | 684 | 68.7 | 618 | 6 | AR388761 | AR388761 Sequence |
| c 17 | 311.5 | 31.3 | 110000 | 1 | AE017225_22 | Continuation (23 o |
| c 18 | 311.5 | 31.3 | 110000 | 1 | AE017334_22 | Continuation (23 o |
| c 19 | 311.5 | 31.3 | 110000 | 1 | AE017355_23 | Continuation (24 o |
| c 20 | 311.5 | 31.3 | 293264 | 1 | AE017031 | AE017031 Bacillus |
| c 21 | 310.5 | 31.2 | 288404 | 1 | AE017272 | AE017272 Bacillus |
| c 22 | 303.5 | 30.5 | 304262 | 1 | AE017005 | AE017005 Bacillus |
| c 23 | 293 | 29.4 | 23738 | 2 | AC020828 | AC020828 Mus muscu |
| 24 | 277.5 | 27.9 | 14140 | 1 | AB015670 | AB015670 Bacillus |
| 25 | 272.5 | 27.4 | 618 | 12 | AY657639 | AY657639 Synthetic |
| c 26 | 272.5 | 27.4 | 11869 | 1 | AE004657 | AE004657 Pseudomon |
| c 27 | 262.5 | 26.4 | 301214 | 1 | AE016786 | AE016786 Pseudomon |
| 28 | 260 | 26.1 | 372 | 6 | AR388768 | AR388768 Sequence |
| c 29 | 258.5 | 26.0 | 310029 | 1 | AE016868 | AE016868 Pseudomon |
| 30 | 256 | 25.7 | 349287 | 1 | BX571860 | BX571860 Photorhab |
| c 31 | 256 | 25.7 | 349980 | 6 | AX770907 | AX770907 Sequence |
| 32 | 250.5 | 25.2 | 636 | 6 | AR386542 | AR386542 Sequence |
| 33 | 244 | 24.5 | 343529 | 1 | CR378676 | CR378676 Photobact |
| 34 | 237.5 | 23.8 | 14305 | 1 | AE014000 | AE014000 Yersinia |
| c 35 | 237.5 | 23.8 | 110000 | 1 | BX950851_45 | Continuation (46 o |
| 36 | 237.5 | 23.8 | 288050 | 1 | AJ414141 | AJ414141 Yersinia |
| 37 | 237.5 | 23.8 | 290029 | 1 | AE017127 | AE017127 Yersinia |
| 38 | 236 | 23.7 | 573 | 6 | AX432019 | AX432019 Sequence |
| 39 | 236 | 23.7 | 344805 | 1 | BX640434 | BX640434 Bordetell |
| 40 | 236 | 23.7 | 346287 | 1 | BX640450 | BX640450 Bordetell |
| c 41 | 235.5 | 23.6 | 294800 | 1 | SME591789 | AL591789 Sinorhizo |
| 42 | 232.5 | 23.3 | 639 | 6 | AR375589 | AR375589 Sequence |
| c 43 | 232.5 | 23.3 | 302650 | 1 | AP005958 | AP005958 Bradyrhiz |

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OM protein - nucleic search, using frame_plus_p2n model

Run on: January 3, 2005, 08:56:05 ; Search time 484 Seconds
(without alignments)
2114.953 Million cell updates/sec

Title: US-10-620-487-2
Perfect score: 996
Sequence: 1 VTPTLLSAFWTYTLITAMTP.....RQLNIVLALLLVYCAVRIFY 195

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlh

Q=/cgn2_1/USPTO_spool/US10620487/runat_29122004_134449_8990/app_query.fasta_1.39
1

-DB=N_Geneseq_23Sep04 -QFMT=fastap -SUFFIX=rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10620487_@CGN_1_1_470_@runat_29122004_134449_8990 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N_Geneseq_23Sep04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*

11: geneseqn2003ds:*
12: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result | No. | Score | % Query Match | Length | DB | ID | Description |
|--------|-----|-------|------------------|--------|----|-------------|--------------------|
| | 1 | 996 | 100.0 | 588 | 3 | AAA52690 | Aaa52690 Escherich |
| | 2 | 996 | 100.0 | 750 | 12 | ADK66005 | Adk66005 E coli yf |
| | 3 | 684 | 68.7 | 618 | 11 | ACH99695 | Ach99695 Klebsiell |
| | 4 | 505 | 50.7 | 1668 | 5 | AAS81979 | Aas81979 DNA encod |
| | 5 | 272.5 | 27.4 | 750 | 11 | ABD10542 | Abd10542 Pseudomon |
| c | 6 | 262.5 | 26.4 | 5040 | 12 | ADQ07624 | Adq07624 DNA seque |
| | 7 | 260 | 26.1 | 372 | 11 | ACH99702 | Ach99702 Klebsiell |
| | 8 | 256 | 25.7 | 609 | 10 | ACF70009 | Acf70009 Photorhab |
| c | 9 | 256 | 25.7 | 110000 | 10 | ACF65385_1 | Continuation (2 of |
| c | 10 | 256 | 25.7 | 110000 | 10 | ACF67367_30 | Continuation (31 o |
| | 11 | 250.5 | 25.2 | 636 | 11 | ACH97476 | Ach97476 Klebsiell |
| | 12 | 236 | 23.7 | 573 | 6 | ABK73143 | Abk73143 Bacillus |
| | 13 | 232.5 | 23.3 | 639 | 10 | ADF00310 | Adf00310 Bacterial |
| | 14 | 228.5 | 22.9 | 636 | 10 | ADF02251 | Adf02251 Bacterial |
| | 15 | 191.5 | 19.2 | 717 | 9 | ADA31709 | Ada31709 DNA encod |
| | 16 | 178 | 17.9 | 726 | 9 | ADA31746 | Ada31746 DNA encod |
| | 17 | 173 | 17.4 | 816 | 11 | ABD17280 | Abd17280 Pseudomon |
| | 18 | 165 | 16.6 | 100 | 8 | ACD79725 | Acd79725 E. coli K |
| | 19 | 165 | 16.6 | 100 | 8 | ACD79727 | Acd79727 E. coli K |
| | 20 | 163.5 | 16.4 | 708 | 9 | ADA32836 | Ada32836 DNA encod |
| | 21 | 162 | 16.3 | 645 | 11 | ACH95100 | Ach95100 Klebsiell |
| | 22 | 161.5 | 16.2 | 618 | 8 | ACA36103 | Aca36103 Prokaryot |
| | 23 | 158.5 | 15.9 | 621 | 11 | ABD03571 | Abd03571 Pseudomon |
| | 24 | 158.5 | 15.9 | 633 | 8 | ACA43829 | Aca43829 Prokaryot |
| c | 25 | 158.5 | 15.9 | 813 | 11 | ABD03188 | Abd03188 Pseudomon |
| | 26 | 157.5 | 15.8 | 618 | 8 | ACA32157 | Aca32157 Prokaryot |
| | 27 | 157.5 | 15.8 | 622 | 5 | AAS93395 | Aas93395 DNA encod |
| | 28 | 157 | 15.8 | 100 | 8 | ACD79726 | Acd79726 E. coli K |
| | 29 | 156.5 | 15.7 | 621 | 8 | ACA53970 | Aca53970 Prokaryot |
| | 30 | 156.5 | 15.7 | 621 | 8 | ACA51728 | Aca51728 Prokaryot |
| | 31 | 156 | 15.7 | 663 | 9 | ADA29490 | Ada29490 DNA encod |
| | 32 | 155.5 | 15.6 | 645 | 9 | ADA30612 | Ada30612 DNA encod |
| | 33 | 155.5 | 15.6 | 714 | 11 | ABD12000 | Abd12000 Pseudomon |
| c | 34 | 155.5 | 15.6 | 816 | 11 | ABD11645 | Abd11645 Pseudomon |
| | 35 | 154 | 15.5 | 633 | 9 | ADA31395 | Ada31395 DNA encod |
| | 36 | 153.5 | 15.4 | 636 | 11 | ABD05572 | Abd05572 Pseudomon |
| c | 37 | 153.5 | 15.4 | 1071 | 11 | ABD05828 | Abd05828 Pseudomon |
| | 38 | 153.5 | 15.4 | 2553 | 11 | ABD05716 | Abd05716 Pseudomon |
| | 39 | 153 | 15.4 | 623 | 8 | ACA48809 | Aca48809 Prokaryot |
| | 40 | 153 | 15.4 | 645 | 11 | ACH96827 | Ach96827 Klebsiell |
| | 41 | 151.5 | 15.2 | 633 | 8 | ACA23772 | Aca23772 Prokaryot |
| | 42 | 149.5 | 15.0 | 753 | 10 | ADF00030 | Adf00030 Bacterial |
| | 43 | 148 | 14.9 | 636 | 11 | ACH96642 | Ach96642 Klebsiell |
| | 44 | 146 | 14.7 | 669 | 9 | ADA31058 | Ada31058 DNA encod |
| | 45 | 143.5 | 14.4 | 639 | 3 | AAA52689 | Aaa52689 Escherich |

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OM protein - nucleic search, using frame_plus_p2n model

Run on: January 3, 2005, 09:06:26 ; Search time 95 Seconds
(without alignments)
1458.988 Million cell updates/sec

Title: US-10-620-487-2
Perfect score: 996
Sequence: 1 VTPTLLSAFWTYTLITAMTP.....RQLNIVLALLLVYCAVRIFY 195

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlh

Q=/cgn2_1/USPTO_spool/US10620487/runat_29122004_134450_9044/app_query.fasta_1.39
1

-DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10620487 @CGN_1_1_69 @runat_29122004_134450_9044 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result | | % | | | | | |
|--------|-------|-------------|--------|----|----------------------|-------------------|--|
| No. | Score | Query Match | Length | DB | ID | Description | |
| 1 | 684 | 68.7 | 618 | 4 | US-09-489-039A-5490 | Sequence 5490, Ap | |
| 2 | 272.5 | 27.4 | 750 | 4 | US-09-252-991A-9146 | Sequence 9146, Ap | |
| 3 | 260 | 26.1 | 372 | 4 | US-09-489-039A-5497 | Sequence 5497, Ap | |
| 4 | 250.5 | 25.2 | 636 | 4 | US-09-489-039A-3271 | Sequence 3271, Ap | |
| 5 | 232.5 | 23.3 | 639 | 4 | US-09-543-681A-595 | Sequence 595, App | |
| 6 | 228.5 | 22.9 | 636 | 4 | US-09-543-681A-2536 | Sequence 2536, Ap | |
| 7 | 191.5 | 19.2 | 717 | 4 | US-09-328-352-2996 | Sequence 2996, Ap | |
| 8 | 178 | 17.9 | 726 | 4 | US-09-328-352-3033 | Sequence 3033, Ap | |
| 9 | 173 | 17.4 | 816 | 4 | US-09-252-991A-15884 | Sequence 15884, A | |
| 10 | 163.5 | 16.4 | 708 | 4 | US-09-328-352-4123 | Sequence 4123, Ap | |
| 11 | 162 | 16.3 | 645 | 4 | US-09-489-039A-895 | Sequence 895, App | |
| 12 | 158.5 | 15.9 | 621 | 4 | US-09-252-991A-2175 | Sequence 2175, Ap | |
| c 13 | 158.5 | 15.9 | 813 | 4 | US-09-252-991A-1792 | Sequence 1792, Ap | |
| 14 | 156 | 15.7 | 663 | 4 | US-09-328-352-777 | Sequence 777, App | |
| 15 | 155.5 | 15.6 | 645 | 4 | US-09-328-352-1899 | Sequence 1899, Ap | |
| 16 | 155.5 | 15.6 | 714 | 4 | US-09-252-991A-10604 | Sequence 10604, A | |
| c 17 | 155.5 | 15.6 | 816 | 4 | US-09-252-991A-10249 | Sequence 10249, A | |
| 18 | 154 | 15.5 | 633 | 4 | US-09-328-352-2682 | Sequence 2682, Ap | |
| 19 | 153.5 | 15.4 | 636 | 4 | US-09-252-991A-4176 | Sequence 4176, Ap | |
| c 20 | 153.5 | 15.4 | 1071 | 4 | US-09-252-991A-4432 | Sequence 4432, Ap | |
| 21 | 153.5 | 15.4 | 2553 | 4 | US-09-252-991A-4320 | Sequence 4320, Ap | |
| 22 | 153 | 15.4 | 645 | 4 | US-09-489-039A-2622 | Sequence 2622, Ap | |
| 23 | 149.5 | 15.0 | 753 | 4 | US-09-543-681A-315 | Sequence 315, App | |
| 24 | 148 | 14.9 | 636 | 4 | US-09-489-039A-2437 | Sequence 2437, Ap | |
| 25 | 146 | 14.7 | 669 | 4 | US-09-328-352-2345 | Sequence 2345, Ap | |
| 26 | 138.5 | 13.9 | 660 | 4 | US-09-489-039A-560 | Sequence 560, App | |
| c 27 | 137 | 13.8 | 269223 | 4 | US-09-596-002-41 | Sequence 41, Appl | |
| 28 | 132 | 13.3 | 489 | 4 | US-09-252-991A-15914 | Sequence 15914, A | |
| 29 | 132 | 13.3 | 627 | 4 | US-09-328-352-985 | Sequence 985, App | |
| 30 | 128.5 | 12.9 | 687 | 4 | US-09-543-681A-682 | Sequence 682, App | |
| 31 | 128.5 | 12.9 | 723 | 4 | US-09-328-352-3411 | Sequence 3411, Ap | |
| 32 | 128.5 | 12.9 | 1200 | 3 | US-09-396-357-1 | Sequence 1, Appli | |
| 33 | 128 | 12.9 | 663 | 4 | US-09-543-681A-373 | Sequence 373, App | |
| 34 | 127 | 12.8 | 603 | 4 | US-09-328-352-647 | Sequence 647, App | |
| 35 | 125.5 | 12.6 | 645 | 4 | US-09-328-352-2569 | Sequence 2569, Ap | |
| 36 | 123.5 | 12.4 | 687 | 4 | US-09-252-991A-7266 | Sequence 7266, Ap | |
| 37 | 123.5 | 12.4 | 834 | 4 | US-09-252-991A-6447 | Sequence 6447, Ap | |
| c 38 | 123.5 | 12.4 | 1521 | 4 | US-09-252-991A-7437 | Sequence 7437, Ap | |
| 39 | 123.5 | 12.4 | 2397 | 4 | US-09-252-991A-7203 | Sequence 7203, Ap | |
| 40 | 122.5 | 12.3 | 606 | 4 | US-09-328-352-2283 | Sequence 2283, Ap | |
| c 41 | 121 | 12.1 | 930 | 4 | US-09-252-991A-6103 | Sequence 6103, Ap | |
| 42 | 115.5 | 11.6 | 783 | 4 | US-09-252-991A-9421 | Sequence 9421, Ap | |
| 43 | 115.5 | 11.6 | 1596 | 4 | US-09-252-991A-9478 | Sequence 9478, Ap | |
| c 44 | 115.5 | 11.6 | 1650 | 4 | US-09-252-991A-9352 | Sequence 9352, Ap | |
| 45 | 112.5 | 11.3 | 750 | 4 | US-09-328-352-1687 | Sequence 1687, Ap | |

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OM protein - nucleic search, using frame_plus_p2n model

Run on: January 3, 2005, 09:05:27 ; Search time 531 Seconds
(without alignments)
2074.218 Million cell updates/sec

Title: US-10-620-487-2
Perfect score: 996
Sequence: 1 VTPTLLSAFWTYTLITAMTP.....RQLNIVLALLLVYCAVRIFY 195

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4176236 seqs, 2824127955 residues

Total number of hits satisfying chosen parameters: 8352472

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlh

Q=/cgn2_1/USPTO_spool/US10620487/runat_29122004_134450_9020/app_query.fasta_1.39
1

-DB=Published_Applications_NA -QFMT=fastap -SUFFIX=rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US10620487_@CGN_1_1_480_@runat_29122004_134450_9020
-NCPU=6 -ICPU=3 -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published_Applications_NA:*
1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*

11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
 13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
 14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
 15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
 16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
 17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
 18: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
 19: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
 20: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
 21: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

| Result | | | % | | | | Description |
|--------|-----|-------|-------|---------|----|----------------------|-------------------|
| | No. | Score | Match | Length | DB | ID | |
| | 1 | 996 | 100.0 | 750 | 16 | US-10-620-487-1 | Sequence 1, Appli |
| | 2 | 236 | 23.7 | 573 | 9 | US-09-974-300-434 | Sequence 434, App |
| | 3 | 161.5 | 16.2 | 618 | 16 | US-10-282-122A-23973 | Sequence 23973, A |
| | 4 | 158.5 | 15.9 | 633 | 16 | US-10-282-122A-31699 | Sequence 31699, A |
| | 5 | 157.5 | 15.8 | 618 | 16 | US-10-282-122A-20027 | Sequence 20027, A |
| | 6 | 156.5 | 15.7 | 621 | 16 | US-10-282-122A-39598 | Sequence 39598, A |
| | 7 | 156.5 | 15.7 | 621 | 16 | US-10-282-122A-41840 | Sequence 41840, A |
| | 8 | 153 | 15.4 | 623 | 16 | US-10-282-122A-36679 | Sequence 36679, A |
| | 9 | 151.5 | 15.2 | 633 | 16 | US-10-282-122A-11642 | Sequence 11642, A |
| | 10 | 142 | 14.3 | 651 | 15 | US-10-156-761-3368 | Sequence 3368, Ap |
| c | 11 | 142 | 14.3 | 9025608 | 15 | US-10-156-761-1 | Sequence 1, Appli |
| | 12 | 137.5 | 13.8 | 618 | 16 | US-10-282-122A-40780 | Sequence 40780, A |
| c | 13 | 137 | 13.8 | 269223 | 16 | US-10-672-787-41 | Sequence 41, Appl |
| | 14 | 129.5 | 13.0 | 543 | 16 | US-10-282-122A-8689 | Sequence 8689, Ap |
| | 15 | 128.5 | 12.9 | 1200 | 9 | US-09-927-395-1 | Sequence 1, Appli |
| | 16 | 128.5 | 12.9 | 1200 | 9 | US-09-847-392-1 | Sequence 1, Appli |
| | 17 | 123.5 | 12.4 | 630 | 16 | US-10-282-122A-30630 | Sequence 30630, A |
| | 18 | 123 | 12.3 | 2731748 | 17 | US-10-297-465A-1 | Sequence 1, Appli |
| | 19 | 118.5 | 11.9 | 792 | 10 | US-09-746-660A-13 | Sequence 13, Appl |
| c | 20 | 118.5 | 11.9 | 3309400 | 9 | US-09-738-626-1 | Sequence 1, Appli |
| | 21 | 117.5 | 11.8 | 630 | 16 | US-10-282-122A-33154 | Sequence 33154, A |
| | 22 | 116.5 | 11.7 | 669 | 9 | US-09-738-626-2570 | Sequence 2570, Ap |
| | 23 | 112 | 11.2 | 621 | 9 | US-09-738-626-2918 | Sequence 2918, Ap |
| c | 24 | 112 | 11.2 | 85692 | 16 | US-10-461-194-1 | Sequence 1, Appli |
| c | 25 | 111 | 11.1 | 86941 | 16 | US-10-461-194-2 | Sequence 2, Appli |
| | 26 | 110.5 | 11.1 | 615 | 15 | US-10-156-761-3747 | Sequence 3747, Ap |
| | 27 | 109.5 | 11.0 | 627 | 16 | US-10-282-122A-14918 | Sequence 14918, A |
| | 28 | 108 | 10.8 | 3309400 | 9 | US-09-738-626-1 | Sequence 1, Appli |
| | 29 | 107.5 | 10.8 | 672 | 15 | US-10-156-761-246 | Sequence 246, App |
| c | 30 | 106.5 | 10.7 | 2731748 | 17 | US-10-297-465A-1 | Sequence 1, Appli |
| | 31 | 104.5 | 10.5 | 1830121 | 14 | US-10-329-960-1 | Sequence 1, Appli |
| | 32 | 104.5 | 10.5 | 1830121 | 16 | US-10-329-670-1 | Sequence 1, Appli |
| | 33 | 104.5 | 10.5 | 1830121 | 18 | US-10-158-865-1 | Sequence 1, Appli |
| | 34 | 104 | 10.4 | 678 | 9 | US-09-738-626-165 | Sequence 165, App |
| | 35 | 98.5 | 9.9 | 417 | 15 | US-10-287-274-274 | Sequence 274, App |
| | 36 | 98.5 | 9.9 | 417 | 16 | US-10-282-122A-6496 | Sequence 6496, Ap |

| | | | | | | | |
|---|----|------|-----|---------|----|----------------------|-------------------|
| | 37 | 96 | 9.6 | 853 | 17 | US-10-767-795-5271 | Sequence 5271, Ap |
| | 38 | 96 | 9.6 | 2847 | 17 | US-10-437-963-58805 | Sequence 58805, A |
| | 39 | 95.5 | 9.6 | 1419 | 16 | US-10-282-122A-25105 | Sequence 25105, A |
| | 40 | 95 | 9.5 | 1611 | 16 | US-10-282-122A-31927 | Sequence 31927, A |
| c | 41 | 95 | 9.5 | 6357 | 18 | US-10-859-149-2 | Sequence 2, Appli |
| c | 42 | 95 | 9.5 | 1163020 | 16 | US-10-398-221-10 | Sequence 10, Appl |
| c | 43 | 95 | 9.5 | 3011208 | 16 | US-10-398-221-2058 | Sequence 2058, Ap |
| | 44 | 94 | 9.4 | 1881 | 15 | US-10-369-493-27537 | Sequence 27537, A |
| | 45 | 93.5 | 9.4 | 822 | 10 | US-09-746-660A-51 | Sequence 51, Appl |

OM protein - protein search, using sw model

Run on: January 3, 2005, 08:48:36 ; Search time 24 Seconds
 (without alignments)
 781.761 Million cell updates/sec

Title: US-10-620-487-2
 Perfect score: 996
 Sequence: 1 VTPTLLSAFWTYTLITAMTP.....RQLNIVLALLLVYCAVRIFY 195

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : PIR_79:*
 1: pirl:*
 2: pir2:*
 3: pir3:*
 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Match | Query Length | DB | ID | Description |
|------------|-------|---------|--------------|----|--------|--------------------------------|
| 1 | 993 | 99.7 | 195 | 2 | A65036 | SEQ Blatner hypothetical 21.2 |
| 2 | 979 | 98.3 | 195 | 2 | D91059 | SEQ Hayashi hypothetical prote |
| 3 | 979 | 98.3 | 195 | 2 | B85904 | SEQ Perna hypothetical prote |
| 4 | 884 | 88.8 | 195 | 2 | AF0830 | SEQ Parkhill probable membrane |
| 5 | 272.5 | 27.4 | 205 | 2 | B83356 | SEQ conserved hypothet |
| 6 | 235.5 | 23.6 | 200 | 2 | AI0022 | probable ABC-trans |
| 7 | 172 | 17.3 | 204 | 2 | B82166 | conserved hypothet |
| 8 | 169 | 17.0 | 222 | 2 | E87264 | efflux protein, Ly |
| 9 | 165.5 | 16.6 | 206 | 2 | B91223 | homoserine/homoser |
| 10 | 164 | 16.5 | 205 | 2 | AI2614 | RhtB family transp |
| 11 | 164 | 16.5 | 224 | 2 | H97396 | dihydrodipicolinat |
| 12 | 163 | 16.4 | 210 | 2 | E87252 | efflux protein, Ly |
| 13 | 162.5 | 16.3 | 249 | 2 | AG3485 | homoserine/homoser |

| | | | | | | |
|----|-------|------|-----|---|--------|--------------------|
| 14 | 160.5 | 16.1 | 222 | 2 | F82353 | conserved hypothet |
| 15 | 158.5 | 15.9 | 197 | 2 | B83280 | hypothetical prote |
| 16 | 158.5 | 15.9 | 216 | 2 | C55580 | hypothetical prote |
| 17 | 158 | 15.9 | 210 | 2 | D84016 | hypothetical prote |
| 18 | 156.5 | 15.7 | 206 | 2 | AF0917 | homoserine/homoser |
| 19 | 156.5 | 15.7 | 206 | 2 | AG0466 | probable homoserin |
| 20 | 156.5 | 15.7 | 235 | 2 | AD2904 | RhtB family transp |
| 21 | 156.5 | 15.7 | 235 | 2 | F97679 | hypothetical prote |
| 22 | 155.5 | 15.6 | 209 | 2 | E82388 | conserved hypothet |
| 23 | 155.5 | 15.6 | 216 | 2 | F83051 | conserved hypothet |
| 24 | 154.5 | 15.5 | 207 | 2 | D83187 | hypothetical prote |
| 25 | 153 | 15.4 | 212 | 2 | H87498 | LysE family transl |
| 26 | 143.5 | 14.4 | 212 | 2 | F64940 | hypothetical prote |
| 27 | 143 | 14.4 | 212 | 2 | AF2805 | homoserine/homoser |
| 28 | 143 | 14.4 | 273 | 2 | F97584 | hypothetical prote |
| 29 | 142.5 | 14.3 | 212 | 2 | G85790 | hypothetical prote |
| 30 | 140.5 | 14.1 | 212 | 2 | C90942 | hypothetical prote |
| 31 | 139 | 14.0 | 212 | 2 | AD0714 | probable membrane |
| 32 | 137.5 | 13.8 | 205 | 2 | G82358 | conserved hypothet |
| 33 | 135.5 | 13.6 | 278 | 2 | E98301 | hypothetical prote |
| 34 | 134.5 | 13.5 | 210 | 2 | AC2982 | RhtB family transp |
| 35 | 130 | 13.1 | 207 | 2 | E83703 | hypothetical prote |
| 36 | 129 | 13.0 | 208 | 2 | C82471 | conserved hypothet |
| 37 | 123.5 | 12.4 | 206 | 2 | C82979 | hypothetical prote |
| 38 | 123.5 | 12.4 | 209 | 2 | C82990 | hypothetical prote |
| 39 | 123 | 12.3 | 213 | 2 | C82523 | amino acid transpo |
| 40 | 122.5 | 12.3 | 205 | 2 | AH3641 | transporter, lysE |
| 41 | 122 | 12.2 | 206 | 2 | C82139 | conserved hypothet |
| 42 | 122 | 12.2 | 216 | 2 | A97675 | amino acid efflux- |
| 43 | 120 | 12.0 | 208 | 2 | G87305 | efflux protein, Ly |
| 44 | 119.5 | 12.0 | 204 | 2 | B82410 | conserved hypothet |
| 45 | 119.5 | 12.0 | 208 | 2 | G84086 | dihydrodipicolinat |

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: January 3, 2005, 08:57:56 ; Search time 3043 Seconds
(without alignments)
2335.113 Million cell updates/sec

Title: US-10-620-487-2
Perfect score: 996
Sequence: 1 VTPTLLSAFWTYTLITAMTP.....RQLNIVLALLLVYCAVRIFY 195

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlh

Q=/cgn2_1/USPTO_spool/US10620487/runat_29122004_134449_9010/app_query.fasta_1.39
1

-DB=EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10620487 @CGN_1_1_3437 @runat_29122004_134449_9010 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result | No. | Score | Query Match | Length | DB | ID | Description |
|--------|-----|-------|-------------|--------|----|----------|--------------------|
| c | 1 | 617 | 61.9 | 681 | 6 | CA366654 | CA366654 642278 NC |
| | 2 | 501 | 50.3 | 856 | 9 | CL650636 | CL650636 PRI0110a |
| | 3 | 464 | 46.6 | 791 | 9 | CL688782 | CL688782 PRI014b |
| | 4 | 451 | 45.3 | 736 | 9 | CL688905 | CL688905 PRI014d |
| c | 5 | 311.5 | 31.3 | 819 | 8 | BH447440 | BH447440 BOHQB49TF |
| c | 6 | 219.5 | 22.0 | 862 | 9 | CL666889 | CL666889 PRI0153c |
| | 7 | 217 | 21.8 | 420 | 8 | BH374397 | BH374397 AG-ND-180 |
| c | 8 | 202.5 | 20.3 | 1233 | 8 | BZ579504 | BZ579504 msh2_6385 |
| | 9 | 200 | 20.1 | 450 | 8 | BH379453 | BH379453 AG-ND-163 |
| c | 10 | 199 | 20.0 | 118 | 6 | CA374430 | CA374430 648800 NC |
| c | 11 | 198.5 | 19.9 | 511 | 6 | CD093163 | CD093163 MC1-0105T |
| c | 12 | 165.5 | 16.6 | 665 | 9 | AG613339 | AG613339 Escherich |
| | 13 | 165.5 | 16.6 | 818 | 9 | CL669909 | CL669909 PRI0160c |
| c | 14 | 162.5 | 16.3 | 863 | 9 | CL689879 | CL689879 PRI0152b |
| c | 15 | 149 | 15.0 | 784 | 8 | BZ577923 | BZ577923 msh2_5638 |
| c | 16 | 137.5 | 13.8 | 1018 | 8 | BZ561476 | BZ561476 pacs2-164 |
| | 17 | 121.5 | 12.2 | 770 | 8 | BZ573390 | BZ573390 msh2_3082 |
| | 18 | 120 | 12.0 | 237 | 2 | AW802587 | AW802587 IL5-UM007 |
| | 19 | 115.5 | 11.6 | 443 | 4 | BG038404 | BG038404 dg34h08.y |
| c | 20 | 111.5 | 11.2 | 798 | 9 | CNS01QYA | AL156722 Anopheles |
| c | 21 | 110.5 | 11.1 | 407 | 8 | AZ576789 | AZ576789 01a12 Sho |
| | 22 | 110.5 | 11.1 | 428 | 2 | BF614897 | BF614897 dg18a02.y |
| c | 23 | 109 | 10.9 | 829 | 8 | BZ549776 | BZ549776 pacs1-60 |
| c | 24 | 108 | 10.8 | 1014 | 8 | BZ558389 | BZ558389 pacs1-60 |
| c | 25 | 106 | 10.6 | 799 | 7 | CN823350 | CN823350 Oa_splbn |
| c | 26 | 105 | 10.5 | 1244 | 2 | BF981306 | BF981306 602308552 |
| | 27 | 101.5 | 10.2 | 881 | 8 | BZ549402 | BZ549402 pacs1-60 |
| | 28 | 101 | 10.1 | 1239 | 8 | BZ555841 | BZ555841 pacs1-60 |
| | 29 | 101 | 10.1 | 1932 | 9 | CG756745 | CG756745 P051-4-F0 |
| c | 30 | 100 | 10.0 | 1299 | 2 | BE966761 | BE966761 601661261 |
| c | 31 | 99.5 | 10.0 | 774 | 5 | BU961093 | BU961093 AGENCOURT |
| c | 32 | 99.5 | 10.0 | 1012 | 9 | CL119129 | CL119129 ISB1-75N6 |
| c | 33 | 99.5 | 10.0 | 1068 | 9 | AG078894 | AG078894 Pan trogl |
| | 34 | 99 | 9.9 | 614 | 7 | CO536048 | CO536048 tail0f08. |
| | 35 | 98 | 9.8 | 562 | 8 | AQ365906 | AQ365906 nbxb0064N |
| c | 36 | 98 | 9.8 | 1151 | 2 | BF037237 | BF037237 601460948 |
| c | 37 | 97 | 9.7 | 1112 | 4 | BI763871 | BI763871 603049636 |
| c | 38 | 97 | 9.7 | 1690 | 2 | BF128393 | BF128393 601810283 |
| c | 39 | 97 | 9.7 | 1823 | 4 | BG253780 | BG253780 602366662 |
| c | 40 | 95.5 | 9.6 | 621 | 8 | AZ452242 | AZ452242 1M0252D04 |
| | 41 | 95.5 | 9.6 | 641 | 7 | CN222730 | CN222730 RJA088F06 |
| c | 42 | 95.5 | 9.6 | 649 | 8 | AZ649701 | AZ649701 1M0519P23 |
| c | 43 | 95.5 | 9.6 | 1623 | 2 | BF131641 | BF131641 601820464 |
| c | 44 | 95 | 9.5 | 1745 | 9 | CL512730 | CL512730 SAIL_866 |
| c | 45 | 94.5 | 9.5 | 723 | 4 | BJ502772 | BJ502772 BJ502772 |

OM protein - protein search, using sw model

Run on: January 3, 2005, 07:58:40 ; Search time 106 Seconds
(without alignments)
1058.472 Million cell updates/sec

Title: US-10-620-487-2
Perfect score: 996
Sequence: 1 VTPTLLSAFWTYTLITAMTP.....RQLNIVLALLLVYCAVRIFY 195

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Match | Query Length | DB | ID | Description |
|------------|-------|---------|--------------|----|------------|--------------------|
| 1 | 993 | 99.7 | 195 | 1 | YFIK_ECOLI | P38101 escherichia |
| 2 | 989 | 99.3 | 195 | 2 | Q8FF11 | Q8ff11 escherichia |
| 3 | 987 | 99.1 | 195 | 2 | Q7C0E0 | Q7c0e0 shigella fl |
| 4 | 987 | 99.1 | 195 | 2 | Q83K22 | Q83k22 shigella fl |
| 5 | 979 | 98.3 | 195 | 2 | Q7ABJ3 | Q7abj3 escherichia |
| 6 | 979 | 98.3 | 195 | 2 | Q8XA19 | Q8xa19 escherichia |
| 7 | 884 | 88.8 | 195 | 2 | Q8Z4J7 | Q8z4j7 salmonella |
| 8 | 884 | 88.8 | 195 | 2 | Q8ZMX5 | Q8zmx5 salmonella |
| 9 | 367.5 | 36.9 | 200 | 2 | Q7P2H4 | Q7p2h4 fusobacteri |
| 10 | 311.5 | 31.3 | 194 | 2 | Q6HIR1 | Q6hir1 bacillus th |
| 11 | 311.5 | 31.3 | 194 | 2 | Q81QH8 | Q81qh8 bacillus an |
| 12 | 311.5 | 31.3 | 194 | 2 | AAT31562 | Aat31562 bacillus |
| 13 | 310.5 | 31.2 | 194 | 2 | Q738B5 | Q738b5 bacillus ce |
| 14 | 310.5 | 31.2 | 194 | 2 | AAS41397 | Aas41397 bacillus |
| 15 | 303.5 | 30.5 | 194 | 2 | Q81DI7 | Q81di7 bacillus ce |

| | | | | | | |
|----|-------|------|-----|---|----------|--------------------|
| 16 | 277.5 | 27.9 | 198 | 2 | O82971 | O82971 bacillus sp |
| 17 | 272.5 | 27.4 | 205 | 2 | Q9I1G9 | Q9ilg9 pseudomonas |
| 18 | 262.5 | 26.4 | 209 | 2 | Q88HF4 | Q88hf4 pseudomonas |
| 19 | 258.5 | 26.0 | 202 | 2 | Q87ZH7 | Q87zh7 pseudomonas |
| 20 | 256 | 25.7 | 202 | 2 | Q7N9E0 | Q7n9e0 photorhabdu |
| 21 | 244 | 24.5 | 204 | 2 | Q6LKF4 | Q6lkf4 photobacter |
| 22 | 244 | 24.5 | 204 | 2 | CAG22196 | Cag22196 photobact |
| 23 | 237.5 | 23.8 | 200 | 2 | Q6CZU2 | Q6czu2 erwinia car |
| 24 | 236 | 23.7 | 219 | 2 | Q7W450 | Q7w450 bordetella |
| 25 | 236 | 23.7 | 219 | 2 | Q7WFK7 | Q7wfk7 bordetella |
| 26 | 235.5 | 23.6 | 197 | 2 | Q92NS0 | Q92ns0 rhizobium m |
| 27 | 235.5 | 23.6 | 200 | 2 | Q8ZJD2 | Q8zjd2 yersinia pe |
| 28 | 234.5 | 23.5 | 192 | 2 | Q8CK91 | Q8ck91 yersinia pe |
| 29 | 234.5 | 23.5 | 192 | 2 | AAS60457 | Aas60457 yersinia |
| 30 | 232.5 | 23.3 | 202 | 2 | Q89G49 | Q89g49 bradyrhizob |
| 31 | 232 | 23.3 | 219 | 2 | Q7VSL5 | Q7vsl5 bordetella |
| 32 | 231 | 23.2 | 196 | 2 | Q7QMF4 | Q7qmf4 anopheles g |
| 33 | 222.5 | 22.3 | 197 | 2 | Q8EG90 | Q8eg90 shewanella |
| 34 | 221 | 22.2 | 193 | 2 | Q88HC2 | Q88hc2 pseudomonas |
| 35 | 215.5 | 21.6 | 199 | 2 | Q8D574 | Q8d574 vibrio vuln |
| 36 | 214.5 | 21.5 | 188 | 2 | Q882W8 | Q882w8 pseudomonas |
| 37 | 213.5 | 21.4 | 198 | 2 | Q98KK8 | Q98kk8 rhizobium l |
| 38 | 211.5 | 21.2 | 200 | 2 | Q6LVD7 | Q6lvd7 photobacter |
| 39 | 211.5 | 21.2 | 200 | 2 | CAG18738 | Cag18738 photobact |
| 40 | 211.5 | 21.2 | 206 | 2 | Q7NWS8 | Q7nws8 chromobacte |
| 41 | 206.5 | 20.7 | 208 | 2 | Q7NWP5 | Q7nwp5 chromobacte |
| 42 | 206 | 20.7 | 195 | 2 | Q7MG87 | Q7mg87 vibrio vuln |
| 43 | 204.5 | 20.5 | 248 | 2 | Q7WDP6 | Q7wdp6 bordetella |
| 44 | 202 | 20.3 | 195 | 2 | Q8D4N7 | Q8d4n7 vibrio vuln |
| 45 | 199.5 | 20.0 | 208 | 2 | Q7W2P8 | Q7w2p8 bordetella |